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## RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/505,377

TIME: 15:18:41

Input Set : A:\230295.sequence listing.txt

Output Set: N:\CRF4\08262004\J505377.raw

3 <110> APPLICANT: LOBANENKOV, VICTOR V  
4 LOUKINOV, DMITRI I  
5 MORSE, HERBERT C  
7 <120> TITLE OF INVENTION: BROTHER OF THE REGULATOR OF IMPRINTED SITES (BORIS)  
9 <130> FILE REFERENCE: 230295  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/505,377  
C--> 11 <141> CURRENT FILING DATE: 2004-08-19  
11 <150> PRIOR APPLICATION NUMBER: PCT/US03/05186  
12 <151> PRIOR FILING DATE: 2003-02-21  
14 <150> PRIOR APPLICATION NUMBER: US 60/358,889  
15 <151> PRIOR FILING DATE: 2002-02-22  
17 <160> NUMBER OF SEQ ID NOS: 49  
19 <170> SOFTWARE: PatentIn version 3.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 3541  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Homo sapiens  
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29 gaggcagagc cacaagccaa agacggagtg gcccgagcat tccggccacg ccttccgcgg 120  
31 ccaagtcatt atggcagcca ctgagatctc tgtcctttct gagcaattca ccaagatcaa 180  
33 agaactcgag ttgatgccgg aaaaaggcct gaaggaggag gaaaaagacg gagtgtgcag 240  
35 agagaaagac catcggagcc ctagtgaagt ggaggccgag cgtacctctg gggccttcca 300  
37 ggacagcgtc ctggaggaag aagtggagct ggtgctggcc ccctcggagg agagcgagaa 360  
39 gtacatcctg accctgcaga cgggtgcact cacttctgaa gctgtggagt tgcaggatat 420  
41 gagcttgctg agcatacagc agcaagaagg ggtgcagggt gtggtgcaac agcctggccc 480  
43 tgggttgctg tggcttgagg aagggccccg gcagagcctg cagcagtggt tggccattag 540  
45 tatccagcaa gagctgtact ccccgcaaga gatggagggt ttgcagttcc acgctctaga 600  
47 ggagaatgtg atggtggcca gtgaagacag taagttagcg gtgagcctgg ctgaaactgc 660  
49 tggactgatc aagctcgagg aagagcagga gaagaaccag ttattggctg aaagaacaaa 720  
51 ggagcagctc ttttttgtgg aaacaatgtc aggagatgaa agaagtgacg aaattgttct 780  
53 cacagtttca aattcaaatg tggagaaca agaggatcaa cctacagctg gtcaagcaga 840  
55 tgctgaaaag gccaaatcta caaaaaatca aagaaagaca aaggagcaa aaggaacctt 900  
57 ccactgtgat gtctgcatgt tcacctctc tagaatgtca agttttaatc gtcatatgaa 960  
59 aactcacacc agtgagaagc ctacactgtg tcacctctgc ctgaaaacct tccgtacggg 1020  
61 cactctgctg cggaaccatg ttaacaccca cacaggaacc aggccctaca agtgtaacga 1080  
63 ctgcaacatg gcatttgtca ccagtggaga actcgtccga cacaggcgct ataaacatac 1140  
65 tcatgagaaa ccctttaaat gttccatgtg caagtatgcc agtgtggagg caagtaaat 1200  
67 gaagcgccat gtccgatccc aactgggga gcgcccctt cagtgttgcc agtgcageta 1260  
69 tgccagcaga gatactaca agctgaaacg ccacatgaga acgcactcag gtgagaagcc 1320  
71 ttacgaatgc cacatctgcc acaccgctt caccagagc gggaccatga aaatacatat 1380  
73 tctgcagaaa cagggcgaat atgtcccaaa ataccagtgt cccattgtg ccaccatcat 1440  
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**ENTERED**

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77 gctgaaatgc cgctactggt ctgctgtctt ccatgaacgc tatgccctca ttcagcacca 1560
79 gaaaactcat aagaatgaga agaggttcaa gtgcaaacac tgcagttatg cctgcaagca 1620
81 ggaacgtcat atgaccgctc acattcgtac ccacactgga gagaaacat tcacctgctt 1680
83 ttcttgcaat aaatgtttcc gacagaagca acttctaaac gctcacttca ggaaatacca 1740
85 cgatgcaaat ttcattcccga ctgtttacaa atgctccaag tgtggcaaag gcttttcccg 1800
87 ctggattaac ctgcacagac attcggagaa gtgtggatca ggggaagcaa agtcggctgc 1860
89 ttcaggaaag ggaagaagaa caagaagag gaagcagacc atcctgaagg aagccacaaa 1920
91 gggtcagaag gaagctgcga agggatggaa ggaagccgcg aacggagacg aagctgctgc 1980
93 tgaggaggct tccaccacga agggagaaca gttcccagga gagatgtttc ctgtcgctgc 2040
95 cagagaaacc acagccagag tcaaagagga agtggatgaa ggcgtgacct gtgaaatgct 2100
97 cctcaacacg atggataagt gagagggatt cgggttgctg gttcactgcc cccaattcct 2160
99 aaagcaagtt agaagttttt agcatttaag gtgtgaaatg ctctcaaca cgatggataa 2220
101 gtgagagaga gtcagggtgc atgttactg cccctaattc cttaaagcaag ttagaaattt 2280
103 ttagcatttt ctttgaaaca attaagttca tgacaatgga tgacacaagt ttgaggtagt 2340
105 gtctagaatt gttctcctgt ttgtagctgg atatttcaaa gaaacattgc aggtatttta 2400
107 taaaagtttt aaaccttgaa tgagagggta acacctcaaa cctatggatt cattcacttg 2460
109 atattggcaa ggtggcccac aatgagttag tagtgatttt tggatatttc aaaatagtct 2520
111 agaccagcta gtgcttccac agtcaaagct ggacattttt atgttgcat atatacacc 2580
113 atgatatttc taataatata tggtttttaa cattaaagac aaatgttttt atacaaatga 2640
115 attttctaca aaatttaag ctaccataat gcttttaatt agttctaaat tcaacaaaa 2700
117 aatgttttac tcttataaaa aggaaaactg agtaggaaat gaaatactag attagactag 2760
119 aaaataagga ataaatcgat ttactttgg tataggagca aggttcacct ttagattttt 2820
121 gtattctctt ttaattatgc tcttggcag gtatgaaatt gccctgggta cattccatta 2880
123 ttgcttatta gtatttact ccataaccct ttttctgct aaaactactc tttttatatt 2940
125 tgtaaaataa ttggcagagt gagaagaac ataaatcag ataaggcaaa tgtgtacctg 3000
127 taaggaatth gtactttttc ataatgccca gtgattagtg agtattttcc ttttgccagt 3060
129 tgacaagatt tttccacct cgagcagcgt gagagatgcc tctttaacac ttgaaattca 3120
131 tttctatctg gatacagagg cagatttttc ttcattgctt agttgagcag tttgttttgc 3180
133 tgccaacctg tctccacctt tgtatttcaa gatcattgat aagccctaaa ttcaaattct 3240
135 taagatatgg accttttatt gaaaatatca caagttcaga atccctatac aatgtgaata 3300
137 tgtggaaata atttcccagc aggaagagca ttatattctc tttgtaccag caaattaatt 3360
139 taactcaact cacatgagat ttaaattctg tgggctgtag tatgccatca ttgtgactga 3420
141 attgtgcaa tggtttctta attttttac tgttatttaa agatgtttta cataattcaa 3480
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145 a 3541

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148 &lt;210&gt; SEQ ID NO: 2

149 &lt;211&gt; LENGTH: 663

150 &lt;212&gt; TYPE: PRT

151 &lt;213&gt; ORGANISM: Homo sapiens

153 &lt;400&gt; SEQUENCE: 2

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156 1 5 10 15
159 Lys Glu Leu Glu Leu Met Pro Glu Lys Gly Leu Lys Glu Glu Glu Lys
160 20 25 30
163 Asp Gly Val Cys Arg Glu Lys Asp His Arg Ser Pro Ser Glu Leu Glu
164 35 40 45
167 Ala Glu Arg Thr Ser Gly Ala Phe Gln Asp Ser Val Leu Glu Glu Glu
168 50 55 60
171 Val Glu Leu Val Leu Ala Pro Ser Glu Glu Ser Glu Lys Tyr Ile Leu

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172	65				70				75				80			
175	Thr	Leu	Gln	Thr	Val	His	Phe	Thr	Ser	Glu	Ala	Val	Glu	Leu	Gln	Asp
176					85					90				95		
179	Met	Ser	Leu	Leu	Ser	Ile	Gln	Gln	Gln	Glu	Gly	Val	Gln	Val	Val	Val
180				100					105					110		
183	Gln	Gln	Pro	Gly	Pro	Gly	Leu	Leu	Trp	Leu	Glu	Glu	Gly	Pro	Arg	Gln
184			115					120					125			
187	Ser	Leu	Gln	Gln	Cys	Val	Ala	Ile	Ser	Ile	Gln	Gln	Glu	Leu	Tyr	Ser
188		130					135					140				
191	Pro	Gln	Glu	Met	Glu	Val	Leu	Gln	Phe	His	Ala	Leu	Glu	Glu	Asn	Val
192	145				150						155				160	
195	Met	Val	Ala	Ser	Glu	Asp	Ser	Lys	Leu	Ala	Val	Ser	Leu	Ala	Glu	Thr
196				165					170						175	
199	Ala	Gly	Leu	Ile	Lys	Leu	Glu	Glu	Glu	Gln	Glu	Lys	Asn	Gln	Leu	Leu
200			180					185						190		
203	Ala	Glu	Arg	Thr	Lys	Glu	Gln	Leu	Phe	Phe	Val	Glu	Thr	Met	Ser	Gly
204			195					200					205			
207	Asp	Glu	Arg	Ser	Asp	Glu	Ile	Val	Leu	Thr	Val	Ser	Asn	Ser	Asn	Val
208		210				215						220				
211	Glu	Glu	Gln	Glu	Asp	Gln	Pro	Thr	Ala	Gly	Gln	Ala	Asp	Ala	Glu	Lys
212	225				230						235				240	
215	Ala	Lys	Ser	Thr	Lys	Asn	Gln	Arg	Lys	Thr	Lys	Gly	Ala	Lys	Gly	Thr
216				245					250						255	
219	Phe	His	Cys	Asp	Val	Cys	Met	Phe	Thr	Ser	Ser	Arg	Met	Ser	Ser	Phe
220			260						265					270		
223	Asn	Arg	His	Met	Lys	Thr	His	Thr	Ser	Glu	Lys	Pro	His	Leu	Cys	His
224		275						280					285			
227	Leu	Cys	Leu	Lys	Thr	Phe	Arg	Thr	Val	Thr	Leu	Leu	Arg	Asn	His	Val
228		290				295						300				
231	Asn	Thr	His	Thr	Gly	Thr	Arg	Pro	Tyr	Lys	Cys	Asn	Asp	Cys	Asn	Met
232	305				310						315				320	
235	Ala	Phe	Val	Thr	Ser	Gly	Glu	Leu	Val	Arg	His	Arg	Arg	Tyr	Lys	His
236				325					330						335	
239	Thr	His	Glu	Lys	Pro	Phe	Lys	Cys	Ser	Met	Cys	Lys	Tyr	Ala	Ser	Val
240			340						345					350		
243	Glu	Ala	Ser	Lys	Leu	Lys	Arg	His	Val	Arg	Ser	His	Thr	Gly	Glu	Arg
244			355					360					365			
247	Pro	Phe	Gln	Cys	Cys	Gln	Cys	Ser	Tyr	Ala	Ser	Arg	Asp	Thr	Tyr	Lys
248		370				375						380				
251	Leu	Lys	Arg	His	Met	Arg	Thr	His	Ser	Gly	Glu	Lys	Pro	Tyr	Glu	Cys
252	385				390						395				400	
255	His	Ile	Cys	His	Thr	Arg	Phe	Thr	Gln	Ser	Gly	Thr	Met	Lys	Ile	His
256				405					410						415	
259	Ile	Leu	Gln	Lys	His	Gly	Glu	Asn	Val	Pro	Lys	Tyr	Gln	Cys	Pro	His
260			420						425					430		
263	Cys	Ala	Thr	Ile	Ile	Ala	Arg	Lys	Ser	Asp	Leu	Arg	Val	His	Met	Arg
264			435					440					445			
267	Asn	Leu	His	Ala	Tyr	Ser	Ala	Ala	Glu	Leu	Lys	Cys	Arg	Tyr	Cys	Ser
268		450					455						460			

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271 Ala Val Phe His Glu Arg Tyr Ala Leu Ile Gln His Gln Lys Thr His
272 465 470 475 480
275 Lys Asn Glu Lys Arg Phe Lys Cys Lys His Cys Ser Tyr Ala Cys Lys
276 485 490 495
279 Gln Glu Arg His Met Thr Ala His Ile Arg Thr His Thr Gly Glu Lys
280 500 505 510
283 Pro Phe Thr Cys Leu Ser Cys Asn Lys Cys Phe Arg Gln Lys Gln Leu
284 515 520 525
287 Leu Asn Ala His Phe Arg Lys Tyr His Asp Ala Asn Phe Ile Pro Thr
288 530 535 540
291 Val Tyr Lys Cys Ser Lys Cys Gly Lys Gly Phe Ser Arg Trp Ile Asn
292 545 550 555 560
295 Leu His Arg His Ser Glu Lys Cys Gly Ser Gly Glu Ala Lys Ser Ala
296 565 570 575
299 Ala Ser Gly Lys Gly Arg Arg Thr Arg Lys Arg Lys Gln Thr Ile Leu
300 580 585 590
303 Lys Glu Ala Thr Lys Gly Gln Lys Glu Ala Ala Lys Gly Trp Lys Glu
304 595 600 605
307 Ala Ala Asn Gly Asp Glu Ala Ala Ala Glu Glu Ala Ser Thr Thr Lys
308 610 615 620
311 Gly Glu Gln Phe Pro Gly Glu Met Phe Pro Val Ala Cys Arg Glu Thr
312 625 630 635 640
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316 645 650 655
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324 <211> LENGTH: 2337
325 <212> TYPE: DNA
326 <213> ORGANISM: Mouse
328 <400> SEQUENCE: 3
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333 gtcccttctg ggtacttcac ccagatcaaa gagcagaagt tgaagcctgg agacctagag 180
335 gaggagaaag aggaggacgg ggtacaaaga gtggaagccc aggagggagt tgtcaaggag 240
337 gtggaggccg agaacagttg cctgcttctg gaggccaggg ccccggtgga gacgacagg 300
339 cggatcctga ccctgcaaac ggtgcacctg gagtcccagg atgtgcacct acaggggctg 360
341 ggatggctga gcgtgccaca ctctgaggag ctttcagggg cggtagcaga ggcggaaggc 420
343 atactgcagt tgccatccgt gctgtggctc gaccagagc cccagctcag ccttcagcat 480
345 tgcgtgacgg tcagcatccc ggaagagctg taccaccag aggagctgca gcggatacat 540
347 tttcacctgc tgagagagaa tgtgctaata gccgaggaga acccagagtt aacaccagac 600
349 ttggacgaaa gcacagccct gaaaaagccc gaagaagatg aaaaggacca gctcccgccc 660
351 caggagagaga cagacaagag agaagagagg ttgctccttc tggaaatgaa accaaaagag 720
353 ggaaaagacg acgaaattgt cctgaccatt tcccatctaa gcctcgaaga acagcaagat 780
355 ccaccagcgg ccaatcagac aagtgtgccc ggagccaaag ccgcaaaacc aaaacggcgg 840
357 aggcagacca agggaaagcc tcagagcttt cagtgtgaca cctgcccgtt cacttcctcc 900
359 aagctctcaa ctttcaatcg tcacatcaaa attcacagca atgagaggcc acacctgtgt 960
361 cacctgtgcc tgaaggcctt ccggactgtc actcttctta ggaacctatg gaaccccac 1020
363 acaggaacca ggccccacaa gtgcaggggac tgcgacatgg cgtttgtcac cagcggagaa 1080

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365 ctcgctccggc acaggcggtta caaacacact tatgagaagc ccttcaagtg ctccctgtgc 1140
367 aagtagccca gcgtcgaggc aagcaagatg aagcgtcaca tccggtcaca cacgggtgag 1200
369 cgtcccttcc agtggttgcca gtgtgcttat gccagcaggg actcctacaa gctgaagcgc 1260
371 cacatgagga cacactcagg tgagaagccg tatgaatgtc ccacctgtca cgtccgggttc 1320
373 acccagagcg ggaccatgaa aatccatata gcacagaagc acggagagaa tgtgccccaa 1380
375 tacgagtgtc cccactgtgc caccatcatc gcgaggaaga gcgacctgcg tgtccatctg 1440
377 cgtaacctgc acagccagag cccggaggag atgaagtgcc gatactgtcc cgctggcttc 1500
379 catgagcgct atgccctcat tcagcaccag aggaccacaa agaacgagaa gaagtccaag 1560
381 tgcaagcagt gcgattacgc gtgcaagcag gagcgatgct tgaaggcgca catgcgcatg 1620
383 cacacaggag agaagccctt ctctgcctg gcctgcaaca agcacttccg acagaagcag 1680
385 ctactgaccg tgcacctgag gaagtacat gacccgaact tcgtcccaa tctgcacctg 1740
387 tgctcaagt gtgataaacg tttctccgcg tggagtaacc tgcagagaca cagaaagaag 1800
389 tgtgaccgg agcatgagac gttagcccc aacaaggaca ggagaccagt gacaaggaca 1860
391 caggcctcgg agggagaagc aggacacaag gaaggggagc ctcaagtccc tggggagcag 1920
393 gctctgggccc accaaggaga agcagcgggg agccagagcc cagaccacgg ccttacctgc 1980
395 gagatgatct ttaacatgat ggataagtga tggataagtg agcagtcgtg cctctccgtg 2040
397 cagtggcctc tgggggaaga aaccagttag aaataagttc ccagacacag cacagtgttc 2100
399 tcagagtttg agatagtgtg tagaaatggt tgagagaagg ggaaaaaac cctgcagcta 2160
401 tttccaaaga cttgagtcag agctcgaagt gaaggtgcac atatctgggc cctagcaggt 2220
403 gcccagaatg agtcagggac agattctagg tgatacttat gtccacgggg gctcagacca 2280
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408 &lt;210&gt; SEQ ID NO: 4

409 &lt;211&gt; LENGTH: 636

410 &lt;212&gt; TYPE: PRT

411 &lt;213&gt; ORGANISM: Mouse

413 &lt;400&gt; SEQUENCE: 4

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420 20 25 30
423 Asp Gly Val Gln Arg Val Glu Ala Gln Glu Gly Val Val Lys Glu Val
424 35 40 45
427 Glu Ala Glu Asn Ser Cys Leu Leu Leu Glu Ala Arg Ala Pro Val Glu
428 50 55 60
431 Ser Asp Arg Arg Ile Leu Thr Leu Gln Thr Val His Leu Glu Ser Gln
432 65 70 75 80
435 Asp Val His Leu Gln Gly Leu Gly Trp Leu Ser Val Pro His Ser Glu
436 85 90 95
439 Glu Leu Ser Gly Thr Val Pro Glu Ala Glu Gly Ile Leu Gln Leu Pro
440 100 105 110
443 Ser Val Leu Trp Leu Asp Pro Glu Pro Gln Leu Ser Leu Gln His Cys
444 115 120 125
447 Val Thr Val Ser Ile Pro Glu Glu Leu Tyr Pro Pro Glu Glu Leu Gln
448 130 135 140
451 Arg Ile His Phe His Leu Arg Glu Asn Val Leu Met Ala Glu Glu
452 145 150 155 160
455 Asn Pro Glu Leu Thr Pro Asp Leu Asp Glu Ser Thr Ala Leu Lys Lys
456 165 170 175
459 Pro Glu Glu Asp Glu Lys Asp Gln Leu Pro Pro Gln Gly Glu Thr Asp

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 08/26/2004  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30

Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49

**VERIFICATION SUMMARY**

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Input Set : A:\230295.sequence listing.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date